

10/643,589  
Sequence alignment B  
US-08-633-148-2  
; Sequence 2, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY ESQ., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-00560005  
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; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 340 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-633-148-2

Query Match 84.6%; Score 1807; DB 1; Length 340;  
Best Local Similarity 99.7%; Pred. No. 4.3e-138;  
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAAGTAVGANVVLVLSLWGANVGAQNITARIGEPLVLKCKGAPKKPPQRLWKLNLTGRTEA	60
Db	1	MAAGTAVGANVVLVLSLWGANVGAQNITARIGEPLVLKCKGAPKKPPQRLWKLNLTGRTEA	60
Qy	61	MWVLSPPQGGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRRNGKETHSNRYVRVYQI	120
Db	61	MWVLSPPQGGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRRNGKETHSNRYVRVYQI	120
Qy	121	PGKPEIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH	180
Db	121	PGKPEIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSVKEQTRRH	180
Qy	181	PETGLFTLQSELMTVPARGGDPRPTFSCSFSPLFRHRLRTAPIQPRVWEFVPLEEVQL	240
Db	181	PETGLFTLQSELMTVPARGGDPRPTFSCSFSPLFRHRLRTAPIQPRVWEFVPLEEVQL	240
Qy	241	VVEPEGGA VAPGGIVTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGYTS	300
Db	241	VVEPEGGA VAPGGIVTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGYTS	300
Qy	301	CVATHSSHGPOESRAVSIIEEPGEEGPTAGSVGGSGLGT	340
Db	301	CVATHSSHGPOESRAVSIIEEPGEEGPTAGSVGGSGLGT	340